(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) EP 0 931 833 A2

(12) EUROPEAN PATENT APPLICATION

(43) Date of publication:
28.07.1999 Bulletin 1999/30

(21) Application number: **99100325.2**

(22) Date of filing: **12.01.1999**

(51) Int Cl.[6]: **C12N 15/53**, C12N 9/04, C12P 13/06, C12R 1/15, C12R 1/13

(84) Designated Contracting States:
AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: **12.01.1998 JP 375198**
11.12.1998 JP 35352198

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(54) Method of producing L-serine fermentation

(57) L-serine is produced by cultivating in a medium a coryneform bacterium having L-serine productivity in which an activity of at least one of phosphoserine phosphatase and phosphoserine transaminase is enhanced, preferably, further having introduced therein a gene coding for D-3-phosophoglycerate dehydrogenase in which feedback inhibition by L-serine is desensitizied, allowing L-serine to accumulate in the medium, and collecting the L-serine from the medium.

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EP 0 931 833 A2

Printed by Jouve, 75001 PARIS (FR)

Description

FIELD OF THE INVENTION

[0001] The present invention relates to a method of producing L-serine for use in the production of amino acid mixtures utilized in the field of pharmaceuticals, chemicals, and cosmetics and to coryneform bacteria constituting the method.

BACKGROUND OF THE INVENTION

[0002] As a conventional method of producing L-serine by fermentation, there has been reported the method in which a bacterial strain capable of converting glycine and sugar into L-serine is used in a medium containing 30 g/L of glycine to produce at most 14 g/L of L-serine. The conversion yield of glycine into L-serine by this method amounted to 46% (Kubota K. Agricultural Biological Chemistry, 49, 7-12 (1985)). Using a bacterial strain capable of converting glycine and methanol into L-serine, 53 g/L of L-serine can be produced from 100 g/L of glycine (T. Yoshida et al., Journal of Fermentation and Bioengineering, Vol. 79, No. 2, 181-183, 1995). In the method using a bacterium belonging to the genus Nocardia, it has been known that the L-serine productivity of the bacterium can be improved by breeding those strains resistant to serine hydroxamate, azaserine or the like (Japanese Patent Publication No. 57-1235). However, these methods involve use of glycine that is a precursor of L-serine and include complicated operation and is disadvantageous from the viewpoint of costs.

[0003] As strains that can ferment L-serine directly from a sugar and do not need addition of the precursor of L-serine to the medium, there has been known Corynebacterium glutamicum that is resistant to D-serine, α-methylserine, o-methylserine, isoserine, serine hydroxamate, and 3-chloroalanine but the accumulation of L-serine is as low as 0.8 g/L (Nogei Kagakukaishi, Vol. 48, No. 3, p201-208, 1974). Accordingly, a further strain improvements of are needed for direct fermentation of L-serine on an industrial scale.

[0004] On the other hand, regarding coryneform bacteria, there have been disclosed a vector plasmid that is capable of autonomous replication in the cell and having a drug resistance marker gene (cf. U. S. Patent 4,514,502) and a method of introducing a gene into the cell (Japanese Patent Application Laid-open No. 2-207791), and the possibility of growing L-threonine or L-isoleucine producing bacteria (U. S. Patents 4,452,890 and 4,442,208). Also, regarding the growth of L-lysine producing bacteria, there has been known a technology involving the incorporation of a gene participating in the biosynthesis of L-lysine into a vector plasmid and the amplification of the plasmid in the cell (Japanese Patent Application Laid-open No. 56-160997).

[0005] In the case of Escherichia coli, the enzymes participating in the biosynthesis of L-serine include an enzyme that is susceptible to feedback inhibition relative to L-serine production in the wild type and an example has been known in which the introduction of a mutant gene that has been mutated so that the feedback inhibition could be desensitized resulted in an enhancement in the L-serine (Japanese Patent No. 2584409). As such genes, there has been known specifically 3-PGDH gene (hereafter, the gene coding for 3-PGDH protein will also be referred to "serA").

[0006] Further, in the case of coryneform bacteria, an example has been known in which the amplification of 3-PGDH gene influences the productivity of L-tryptophane (Japanese Patent Application Laid-open No. 3-7591).

SUMMARY OF THE INVENTION

[0007] An object of the present invention is to provide a microorganism that converts a sugar into L-serine and to provide a method of accumulating L-serine in a culture medium utilizing the ability of the microorganism to convert the sugar into L-serine, i.e., a method of producing L-serine that is advantageous in practicing on an industrial scale.

[0008] As a result of intensive investigation with view to achieving the above object, it has now been discovered by the present inventors that screening a strain in which an activity of at least one of phosphoserine phosphatase and phosphoserine transaminase is enhanced from coryneform bacteria having L-serine productivity, preferably the bacteria deficient in L-serine decomposing activity or a mutant thereof having resistance to an L-serine analogue, and L-serine fermentation using the screened strain will enhance the accumulation of L-serine drastically. The present invention has been completed based on this discovery.

[0009] That is, the present invention relates to a coryneform bacterium having L-serine productivity in which an activity of at least one of phosphoserine phosphatase and phosphoserine transaminase is enhanced.

[0010] Further, the present invention relates to the coryneform bacterium as described above, which is enhanced the activitise of both phosphoserine phosphatase and phosphoserine transaminase; the coryneform bacterium as described above, having L-serine productivity due to deficiency in L-serine decomposing activity; the coryneform bacterium as described above, having L-serine productivity due to its resistance to L-serine analogue(s); the coryneform bacterium as described above, in which an activity of phosphoserine phosphatase or phosphoserine transaminase is

enhanced by increasing a copy number of a gene coding for phosphoserine phosphatase or a gene coding for phosphoserine transaminase in the coryneform bacterium described above in its cell; and the coryneform bacterium as described above, having introduced therein a gene coding for D-3-phosophoglycerate dehydrogenase in which feedback inhibition by L-serine is desensitized.

[0011] Further, the present invention relates to a method of producing L-serine, comprising the steps of cultivating the coryneform bacterium as described above in a medium to accumulate L-serine in the medium and collecting the L-serine from the medium.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] Fig. 1 illustrates a manner of feedback inhibition of 3-PGDH derived from various strains by L-serine. The horizontal axis indicates the concentration of L-serine in the enzyme solution. The vertical axis indicates percentage of the 3-PGDH activity in the presence of L-serine to that in the absence of L-serine. Symbol ♦ illustrates a manner of feedback inhibition of 3-PGDH derived from ATCC14067 strain by L-serine. Symbol ■ illustrates a manner of feedback inhibition of 3-PGDH derived from AJ13377 strain by L-serine. Symbol ▲ illustrates a manner of feedback inhibition of 3-PGDH derived from AJ13324 strain by L-serine. Symbol × illustrates a manner of feedback inhibition of 3-PGDH derived from AJ13325 strain by L-serine. Symbol * illustrates a manner of feedback inhibition of 3-PGDH derived from AJ13327 strain by L-serine.

[0013] Fig. 2 illustrates the construction of plasmids pVK7 and pVK6.

[0014] Fig. 3 illustrates the construction of plasmid pSB on which serB is carried.

[0015] Fig. 4 illustrates the construction of plasmid pSC on which serC is carried.

[0016] Fig. 5 illustrates the construction of plasmid pBC8 and pBC14 on which serB and serC are carried.

DETAILED DESCRIPTION OF THE INVENTION

[0017] The coryneform bacteria referred to in the present invention are a group of microorganisms as defined in Bergey's Manual of Determinative Bacteriology, 8th ed., p. 599 (1974), which are aerobic Gram-positive rods having no acid resistance and no spore-forming ability. The coryneform bacteria include bacteria belonging to the genus Corynebacterium, bacteria belonging to the genus Brevibacterium having been hitherto classified into the genus Brevibacterium but united as bacteria belonging to the genus Corynebacterium at present, and bacteria belonging to the genus Brevibacterium closely relative to bacteria belonging to the genus Corynebacterium and bacteria belonging to the genus Microbacterium.

[0018] The coryneform bacteria of the present invention are coryneform bacteria that have L-serine productivity in which an activity of phosphoserine phosphatase or phosphoserine transaminase is enhanced. Such bacteria can be obtained, for example, by increasing the copy number of a gene coding for phosphoserine phosphatase (hereafter, referred to as "serB") or a gene coding for phosphoserine transaminase (hereafter, referred to as "serC") in a coryneform bacterial cell having L-serine productivity.

[0019] Also, the coryneform bacteria of the present invention can be obtained by imparting L-serine productivity to a coryneform bacterium having an enhanced activity of phosphoserine phosphatase or phosphoserine transaminase.

[0020] As the coryneform bacteria having L-serine productivity, there can be cited, for example, coryneform bacterial deficient in L-serine decomposing activity, coryneform bacteria resistant to L-serine analogues, and coryneform bacteria deficient in L-serine decomposing activity and being resistant to L-serine analogues.

[0021] In the present invention, the L-serine analogue includes azaserine or β-(2-thienyl)-DL-alanine.

[0022] The coryneform bacteria resistant to L-serine analogues and having L-serine productivity, more preferably the coryneform bacteria deficient in L-serine decomposing activity from among them can be artificially mutated or induced using wild type or coryneform bacteria having L-serine productivity as a parent strain.

[0023] The coryneform bacteria having resistance to an L-serine analogue, deficient in L-serine decomposing activity, and having L-serine productivity can be collected, for example, as follows. Brevibacterium flavum ATCC14067 is subjected to mutation treatment by a conventional method (contact with N-methyl-N'-nitro-N-nitrosoguanidine, etc.) to obtain a mutant that is deficient in L-serine decomposing activity, and then a bacterium resistant to an L-serine analogue such as azaserine or β-(2-thienyl)-DL-alanine is collected from the mutant as a parent strain. Also, after L-serine analogue-resistant bacterium is obtained, a mutant deficient in L-serine decomposing activity may be obtained. Among the mutants obtained by the methods described above, there are strains that accumulate L-serine in high concentrations.

[0024] The L-serine analogue-resistant bacteria can be obtained by introducing the mutant serA described later on into a parent strain or L-serine decomposing activity deficient mutant.

[0025] By the term "L-serine analogue resistance" is meant the property that a bacterium grows faster than the wild type in a medium containing an L-serine analogue.

[0026] More specifically, for example, the term "azaserine resistance" refers to the property that a bacterium grows faster than the wild type in a medium containing azaserine. For example, those strains that form colonies on a solid medium containing 0.25 g/L of azaserine at 30°C within 4 to 5 days are said to have azaserine resistance.

[0027] Similarly, the term "β-(2-thienyl)-DL-alanine resistance" refers to the property that a bacterium grows faster than the wild type in a medium containing β-(2-thienyl)-DL-alanine. For example, those strains that form colonies on a solid medium containing 0.25 g/L of β-(2-thienyl)-DL-alanine at 30°C within 4 to 5 days are said to have β-(2-thienyl)-DL-alanine resistance.

[0028] Next, the enhancement of phosphoserine phosphatase activity or phosphoserine transaminase activity will be described.

[0029] The enhancement of phosphoserine phosphatase activity or phosphoserine transaminase activity can be performed by introducing serB or serC each in an expressible form into a coryneform bacterium. This is possible either by forced expression of genes coding for respective enzymes by means of separate promoters or by forced expression of the both genes under the control of a single promoter. Regardless of whether these genes are on a plasmid or chromosome, the expression may be enhanced by enhancement of an expression control sequence such as promoter of a gene, or improvement in translation efficiency. Alternatively, the enzyme activity can be enhanced by amplification of the number of genes on a chromosome. Further, the enhancement of these enzyme activities can be achieved by use of a modified gene coding for phosphoserine phosphatase or phosphoserine transaminase modified in such a manner that a modified enzyme having an increased specific activity is coded for.

[0030] In order to introduce serB or serC into a coryneform bacterium, a DNA fragment containing serB or serC may be ligated with a vector that functions in coryneform bacteria to generate a recombinant DNA, followed by introduction of it into a coryneform bacterium host having L-serine productivity to transform it. As a result of an increase in copy number of serB or serC in the cell of transformed strain, the phosphoserine phosphatase activity or phosphoserine transaminase activity thereof is amplified. Introduction of a recombinant DNA containing both serB and serC or both a recombinant DNA containing serB and a recombinant DNA containing serC into a coryneform bacterium will amplify the both phosphoserine phosphatase activity and phosphoserine transaminase activity.

[0031] The base sequences of serB and serC are known (serB: GenBank; X03046 M30784, serC: GenBank; D90728). It is possible to synthesize primers based on their base sequences and collect the serB gene or serC gene of these microorganisms by the PCR method using the chromosomal DNA of Escherichia coli, Brevibacterium flavum or other microorganisms as a template. As such a primer, there can be cited the primer having the base sequence shown in Sequence ID No. 15 to 18.

[0032] It is preferred that serB gene or serC gene is ligated with vector DNA autonomously replicable in cells of Escherichia coli and/or coryneform bacteria to prepare recombinant DNA, and the recombinant DNA is introduced into cells of Escherichia coli beforehand. Such provision makes following operations easy. The vector autonomously replicable in cells of Escherichia coli is preferably a plasmid vector which is preferably autonomously replicable in cells of a host, including, for example, pUC19, pUC18, pBR322, pHSG299, pHSG399, pHSG398, and RSF1010.

[0033] In the case where serB gene and serC gene are loaded on separate vectors for introduction into a coryneform bacterium, it is preferred to use two vectors having respective marker genes differing one from another.

[0034] Recombinant DNA may be prepared by utilizing transposon (WO 02/02627 International Publication Pamphlet, WO 93/18151 International Publication Pamphlet, European Patent Application Laid-open No. 0445385, Japanese Patent Application Laid-open No. 6-46867, Vertes, A. A. et al., Mol. Microbiol., 11, 739-746 (1994), Bonamy, C., et al., Mol. Microbiol., 14, 571-581 (1994), Vertes, A. A. et al., Mol. Gen. Genet., 245, 397-405 (1994), Jagar, W. et al., FEMS Microbiology Letters, 126, 1-6 (1995), Japanese Patent Application Laid-open No. 7-107976, Japanese Patent Application Laid-open No. 7-327680, etc.), phage vectors, recombination of chromosomes (Experiments in Molecular Genetics, Cold Spring Harbor Laboratory Press (1972); Matsuyama, S. and Mizushima, S., J. Bacteriol., 162, 1196 (1985)) and the like.

[0035] When a DNA fragment having an ability to allow a plasmid to be autonomously replicable in coryneform bacteria is inserted into these vectors, they can be used as a so-called shuttle vector autonomously replicable in both Escherichia coli and coryneform bacteria.

[0036] Such a shuttle vector includes the followings. Microorganisms harboring each of vectors and deposition numbers in international deposition facilities are shown in parentheses.

pHC4: Escherichia coli AJ12617 (FERM BP-3532)
pAJ655: Escherichia coli AJ11882 (FERM BP-136) Corynebacterium glutamicum SR8201 (ATCC 39135)
pAJ1844: Escherichia coli AJ11883 (FERM BP-137) Corynebacterium glutamicum SR8202 (ATCC 39136)
pAJ611: Escherichia coli AJ11884 (FERM BP-138)
pAJ3148: Corynebacterium glutamicum SR8203 (ATCC 39137)
pAJ440: Bacillus subtilis AJ11901 (FERM BP-140)

[0037] These vectors are obtainable from the deposited microorganisms as follows. Cells collected at a logarithmic growth phase were lysed by using lysozyme and SDS, followed by separation from a lysate by centrifugation at 30,000 x g to obtain a supernatant to which polyethylene glycol is added, followed by fractionation and purification by means of cesium chloride-ethidium bromide equilibrium density gradient centrifugation.

[0038] Escherichia coli can be transformed by introducing a plasmid in accordance with, for example, a method of D. M. Morrison (Methods in Enzymology, 68, 326 (1979)) or a method in which recipient cells are treated with calcium chloride to increase permeability for DNA (Mandel, M. and Higa, A., J. Mol. Biol., 53, 159 (1970)).

[0039] Introduction of plasmids to coryneform bacteria to cause transformation can be performed by the electric pulse method (Sugimoto et al., Japanese Patent Application Laid-open No. 2-207791).

[0040] Examples of the coryneform bacterium used to introduce the DNA described above include, for example, the following wild type strains:

Corynebacterium acetoacidophilum ATCC 13870;
Corynebacterium acetoglutamicum ATCC 15806;
Corynebacterium callunae ATCC 15991;
Corynebacterium glutamicum ATCC 13032;
(Brevibacterium divaricatum) ATCC 14020;
(Brevibacterium lactofermentum) ATCC 13869;
(Corynebacterium lilium) ATCC 15990;
(Brevibacterium flavum) ATCC 14067;
Corynebacterium melassecola ATCC 17965;
Brevibacterium saccharolyticum ATCC 14066;
Brevibacterium immariophilum ATCC 14068;
Brevibacterium roseum ATCC 13825;
Brevibacterium thiogenitalis ATCC 19240;
Microbacterium ammoniaphilum ATCC 15354;
Corynebacterium thermoaminogenes AJ12340 (FERM BP-1539).

[0041] Enhancement of phosphoserine phosphatase activity or phosphoserine transaminase activity can also be achieved by introducing multiple copies of the serB gene or serC gene into the chromosomal DNA of the above-described host strains. In order to introduce multiple copies of the serB gene or serC gene in the chromosomal DNA of coryneform bacterium, the homologous recombination is carried out using a sequence whose multiple copies exist in the chromosomal DNA as targets. As sequences whose multiple copies exist in the chromosomal DNA, repetitive DNA, inverted repeats exist at the end of a transposable element can be used. Also, as disclosed in Japanese Patent Publication Laid-Open No. 2-109985, it is possible to incorporate the serB gene or serC gene into transposon, and allow it to be transferred to introduce multiple copies of the serB gene or serC gene into the chromosomal DNA. By either method, the number of copies of the serB gene or serC gene within cells of the transformant strain increases, and as a result, phosphoserine phosphatase activity or phosphoserine transaminase activity is enhanced.

[0042] Other than the above-described gene amplification, enhancement of phosphoserine phosphatase activity or phosphoserine transaminase activity can also be achieved by substituting the expression regulation sequence such as promoter of the serB gene or serC gene with a more potent one. For example, lac promoter, trp promoter, trc promoter, tac promoter, and P_R promoter and P_L promoter of lambda phage are known as potent promoters. By substituting the promoter inherent in serB gene or serC gene with these promoters, the expression of serB gene or serC gene is enhanced, thereby enhancing phosphoserine phosphatase activity or phosphoserine transaminase activity.

[0043] In a preferred embodiment, the coryneform bacteria of the present invention is a strain obtained by introducing a gene coding for D-3-phosphoglycerate dehydrogenase (hereafter, also referred to as "3-PGDH") in which feedback inhibition by L-serine is desensitized, into a coryneform bacterium having L-serine productivity and an enhanced activity of phosphoserine phosphatase or phosphoserine transaminase.

[0044] 3-PGDH catalyzes reaction in which 3-phosphoglycerate is oxidized into 3-phosphohydroxylpyruvic acid in the presence of nicotinamide adenine dinucleotide (NAD) as a coenzyme.

[0045] 3-PGDH derived from a wild type coryneform bacterium is susceptible to feedback inhibition by L-serine and its activity is almost completely inhibited in the presence of 10 mM of L-serine. By the term "3-PGDH in which feedback inhibition by L-serine is desensitized" is meant 3-PGDH having 20% or more, preferably 40% or more, more preferably 90% or more of the activity in the absence of L-serine even in the presence of 10 mM of L-serine. 3-PGDH derived from Brevibacterium flavum AJ13327 described in the examples hereinbelow retains substantially 100% of the activity in the presence of 80 mM of L-serine and therefore one of the most preferred 3-PGDHs.

[0046] The gene coding for 3-PGDH in which feedback inhibition by L-serine is desensitized can be prepared from the chromosomal DNA of L-serine analogue resistant coryneform bacteria, for example, azaserine resistant strain

AJ13327 of Brevibacterium flavum obtained in the examples described below.

[0047] 3-PGDH derived from a wild type coryneform bacterium (hereafter, DNA coding for this is also referred to as "wild type serA") has the amino acid sequence described by SEQ ID NO : 12 in the Sequence Listing. Specific examples of the 3-PGDH in which feedback inhibition by L-serine is desensitized (hereafter, DNA coding for this is also referred to as "mutant serA") include D-3-phosphoglycerate dehydrogenase characterized in that in D-3-phosphoglycerate dehydrogenase having the amino acid sequence described by SEQ ID NO : 12 in the Sequence Listing or the same amino acid sequence as above but has substitution, addition or deletion of one or more amino acids, the amino acid residue corresponding to the 325th glutamic acid residue of the amino acid sequence in the SEQ ID NO : 12 has been substituted by other amino acid. Most preferred as the other amino acid residue is a lysine residue.

[0048] The DNA fragment containing serA gene from a coryneform bacterium can be isolated, for example, by preparing chromosomal DNA according to the method of Saito and Miura (H. Saito and K. Miura, Biochem. Biophys. Acta, 72, 619 (1963)) or the like and then amplifying serA gene by polymerase chain reaction method (PCR: polymerase chain reaction; cf. White, T.

[0049] J. et al.; Trends Genet. 5, 185 (1989)). For example, in order to amplify DNA fragment containing ORF (172 to 1705) of SEQ ID NO : 11 in the Sequence Listing, any 20 to 30 bases are selected from the region from the first base in SEQ ID NO : 11 to the base immediately before ATG to obtain one primer. Further, any 20 to 30 bases are selected from the region from the base immediately after the termination codon to the last base in SEQ ID NO : 11 to obtain another primer.

[0050] When serA is isolated from a wild type strain of 3-PGDH, wild type serA is obtained and isolation of serA from a mutant retaining 3-PGDH in which feedback inhibition by L-serine is desensitized (3-PGDH mutant) gives mutant serA. Specifically, the wild type serA has the sequence described by SEQ ID NO : 11 in the Sequence Listing, and mutant serA has the sequence described by SEQ ID NO : 13 in the Sequence Listing.

[0051] The mutant serA may be introduced into a coryneform bacterium by transformation of the coryneform bacterium with a mutant serA-containing recombinant vector in the same manner as in the introduction of serB or serC. The mutant serA is preferably introduced in multiple copies. The mutant serA and serB or serC may be loaded on a single vector or on separate two or three vectors, respectively.

[0052] For L-serine production using the strain of the present invention, the following methods may be used. As the medium to be used, there can be used conventional liquid mediums containing carbon sources, nitrogen sources, inorganic salts, and optionally organic trace nutrients such as amino acids, vitamins, etc., if desired.

[0053] As carbon sources, it is possible to use sugars such as glucose, sucrose, fructose, galactose; saccharified starch solutions, sweet potato molasses, sugar beet molasses and hightest molasses which are including the sugars described above; organic acids such as acetic acid; alcohols such as ethanol; glycerol and the like.

[0054] As nitrogen sources, it is possible to use ammonia gas, aqueous ammonia, ammonium salts, urea, nitrates and the like. Further, organic nitrogen sources for supplemental use, for example, oil cakes, soybean hydrolysate liquids, decomposed casein, other amino acids, corn steep liquor, yeast or yeast extract, peptides such as peptone, and the like, may be used.

[0055] As inorganic ions, phosphoric ion, magnesium ion, calcium ion, iron ion, manganese ion and the like may be added optionally.

[0056] In case of using the microorganism of the present invention which requires nutrients such as amino acids for its growth, the required nutrients should be supplemented.

[0057] The microorganisms are incubated usually under aerobic conditions at pH 5 to 8 and temperature ranges of 25 to 40°C. The pH of the culture medium is controlled at a predetermined value within the above-described ranges depending on the presence or absence of inorganic or organic acids, alkaline substances, urea, calcium carbonate, ammonia gas, and the like.

[0058] L-Serine can be collected from the fermentation liquid, for example, by separating and removing the cells, subjecting to ion exchange resin treatment, concentration cooling crystallization, membrane separation, and other known methods in any suitable combination. In order to remove impurities, activated carbon adsorption and recrystallization may be used for purification.

[0059] The present invention provides a coryneform bacterium that synthesizes L-serine from a sugar. The coryneform bacterium can be utilized in a method of producing L-serine that is advantageous industrially.

DESCRIPTION OF PREFERRED EMBODIMENTS

(Example 1) Construction of L-serine producing bacteria Brevibacterium flavum AJ13324 and AJ13327

[0060] Brevibacterium flavum AJ13324 and AJ13327 were constructed from Brevibacterium flavum AJ13377 that is deficient in L-serine decomposing activity obtained from wild type strain Brevibacterium flavum ATCC 14067.

[0061] To obtain a mutant, cells proliferated for 24 hours in a bouillon medium (a medium containing 1 g of fish meat

extract, 1 g of polypeptone, 0.5 g of yeast extract, and 0.5 g of sodium chloride in 1 liter of water, adjusted to pH 7.0) were suspended in 100 mM phosphate buffer (pH 7.0) (containing 10^9 to 10^{10} cells/ml). NG (N-methyl-N'-nitro-N-nitrosoguanidine) was added to the suspension to a concentration of 200 pg/ml and left to stand at 30°C for 30 minutes. The thus NG treated cells were washed well with the above-described buffer.

[0062] To select strains having no L-serine decomposing activity from the NG treated cells, NG treated cells of Brevibacterium flavum ATCC 14067 after washed were spread on a bouillon agar medium and incubated at 30°C for 24 hours to allow colony formation. Then, the colonies on the bouillon agar medium were used as a negative and replica formation was performed on a minimal medium and a minimal medium for selection. Then, strains were screened that grow on the minimal medium but do not grow on the minimal medium for selection. The minimal medium was a medium that contained 20 g of glucose, 1 g of ammonium sulfate, 1 g of potassium dihydrogen phosphate, 2.5 g of urea, 0.4 g of magnesium sulfate heptahydrate, 0.01 g of iron (II) sulfate heptahydrate, 0.01 g of manganese sulfate tetra- to pentahydrate, 50 μg of biotin, 200 μg of thiamin hydrochloride, 200 pg of nicotinic acid amide, and 2.0 g of agar per liter of distilled water. The minimal medium for selection was a medium that contained 1 g of ammonium sulfate, 1 g of potassium dihydrogen phosphate, 2.5 g of urea, 0.4 g of magnesium sulfate heptahydrate, 0.01 g of iron (II) sulfate heptahydrate, 0.01 g of manganese sulfate tetra- to pentahydrate, 50 pg of biotin, 200 μg of thiamin hydrochloride, 200 μg of nicotinic acid amide, 0.5 g of L-serine and 2.0 g of agar per liter of distilled water. Among the mutants obtained by this method were found many strains that have no L-serine decomposing activity and Brevibacterium flavum AJ13377 was obtained as one of such strains.

[0063] To select azaserine resistant strains from NG treated strains using Brevibacterium flavum AJ13377 as a parent strain, NG treated Brevibacterium flavum AJ13377 cells after washed were inoculated on a minimal medium for selection. The minimal medium for selection was a medium that contained 20 g of glucose, 1 g of ammonium sulfate, 1 g of potassium dihydrogen phosphate, 2.5 g of urea, 0.4 g of magnesium sulfate heptahydrate, 0.01 g of iron (II) sulfate heptahydrate, 0.01 g of manganese sulfate tetra- to pentahydrate, 50 pg of biotin, 200 pg of thiamin hydrochloride, 200 pg of nicotinic acid amide, and 250 mg of azaserine per liter of distilled water. The NG treated mutant was incubated in the above-described medium at 30°C for 5 to 10 days. The cell culture thus obtained was spread on a bouillon agar medium and incubated at 30°C for 24 hours for colony formation. Azaserine resistant strains were obtained from the strains that formed colonies. The mutants thus obtained included many strains that accumulated L-serine in considerable amounts at high yields. From the strains were obtained two strains, i.e., Brevibacterium flavum AJ13324 and AJ13327. It was confirmed that these strains were able to grow in the presence of 0.25 g/L of azaserine.

(Example 2) Construction of novel L-serine producing bacterium Brevibacterium flavum AJ13325

[0064] Brevibacterium flavum AJ13325 was constructed from Brevibacterium flavum AJ13377 lacking L-serine decomposing activity, which was obtained from the wild type strain Brevibacterium flavum ATCC 14067.

[0065] To select β-(2-thienyl)-DL-alanine resistant strains from NG treated strains using Brevibacterium flavum AJ13377 as a parent strain, Brevibacterium flavum AJ13377 cells were NG treated and washed before their inoculation on a minimal medium for selection. The minimal medium for selection was a medium that contained 20 g of glucose, 1 g of ammonium sulfate, 1 g of potassium dihydrogen phosphate, 2.5 g of urea, 0.4 g of magnesium sulfate heptahydrate, 0.01 g of iron (II) sulfate heptahydrate, 0.01 g of manganese sulfate tetra- to pentahydrate, 50 μg of biotin, 200 μg of thiamin hydrochloride, 200 μg of nicotinic acid amide, and 250 mg of β-(2-thienyl)-DL-alanine per liter of distilled water. The NG treated mutant was incubated in the above-described medium at 30°C for 5 to 10 days. The cell culture thus obtained was spread on a bouillon agar medium and incubated at 30°C for 24 hours for colony formation. β-(2-Thienyl)-DL-alanine resistant strains were obtained from the strains that formed colonies. The mutants thus obtained included many strains that accumulated L-serine in considerable amounts at high yields. Brevibacterium flavum AJ13325 was obtained as one of such strains. It was confirmed that these strains were able to grow in the presence of 0.25 g/L of β-(2-thienyl)-DL-alanine.

(Example 3) Production of L-serine by L-serine producing bacteria Brevibacterium flavum AJ13324, AJ13325 and AJ13327

[0066] Brevibacterium flavum AJ13324, AJ13325 and AJ13327 were each incubated on a bouillon agar medium at 30°C for 24 hours and a loopful of each microorganism was inoculated in a 500 ml shaking flask containing 20 ml of a fermentation medium having the composition shown in Table 1. As a control, the parent strains Brevibacterium flavum ATCC 14067 and AJ13377 were inoculated as a same manner as described above. The medium was adjusted to pH 7.0 with potassium hydroxide and autoclaved at 115°C for 15 minutes. After the sterilization and cooling, calcium carbonate that had been dry air sterilized at 180°C for 3 hours was added in an amount of 5 g/L.

Table 1

Component	Content/liter
Glucose	110.0 g
Potassium dihydrogen phosphate	0.4 g
Magnesium sulfate heptahydrate	0.4 g
Iron (II) sulfate heptahydrate	0.01 g
Manganese sulfate tetra- to penta-hydrate	0.01 g
Ammonium sulfate	25.0 g
Thiamin hydrochloride	100 pg
Biotin	100 pg
Soy bean protein hydrochloric acid hydrolysate ("Mieki" (registered trademark)	40 ml
pH	7.0

[0067] Determination of L-serine using high performance liquid chromatography (Hitachi L-8500 Amino Acid Auto-analyzer) revealed that Brevibacterium flavum AJ13324, AJ13325 and AJ13327 accumulated L-serine in the medium in amounts of 15.2 g/L, 14.3 g/L, and 15.4 g/L, respectively. On the other hand, Brevibacterium flavum strains ATCC 14067 and AJ13377 incubated as a control accumulated L-serine in amounts of 0 g/L and 5.0 g/L, respectively.

[0068] The culture broth of Brevibacterium flavum AJ13324 was centrifuged and the supernatant was subjected to desalting treatment using cation exchange resin, followed by chromatographic separation with cation exchange resin and anion exchange resin to remove byproducts and purification by crystallization to obtain L-serine crystals of at least 99% purity at a yield from broth of 55%.

(Example 4) Measurement of 3-PGDH activity

[0069] Brevibacterium flavum AJ13324, AJ13325 and AJ13327 were each incubated on a bouillon agar medium at 30°C for 24 hours and a loopful of each microorganism was inoculated in a 500 ml shaking flask containing 50 ml of a fermentation medium having the composition shown in Table 2. As a control, the parent strains Brevibacterium flavum ATCC 14067 and AJ13377 were inoculated as a same manner as described above. The medium for inoculation was adjusted to pH 5.5 with sodium hydroxide and autoclaved at 115°C for 15 minutes.

Table 2

Component	Content/liter
Glucose	30.0 g
Potassium dihydrogen phosphate	1.0 g
Magnesium sulfate heptahydrate	0.4 g
Iron (II) sulfate heptahydrate	0.01 g
Manganese sulfate tetra- to pentahydrate	0.01 g
Ammonium sulfate	3.0 g
Soy bean protein hydrochloric acid hydrolysate ("Mieki" (registered trademark)	3.0 ml
Thiamin hydrochloride	200 µg
Biotin	50 pg
Urea	3.0 g
Yeast extract	2.0 g
pH	5.5

[0070] After collecting cells from the culture broth of each strain, the cells were washed twice with physiological saline and suspended in 50 mM sodium phosphate buffer (pH 7.0) containing 2 mM dithiothreitol. After ice cooling, the suspension was subjected to a sonicator to fragment the cells and the resulting liquid was ultracentrifuged. The ultracentrifugaton was run at 45,000 rpm for 1 hour to obtain a crude enzyme solution.

[0071] The enzyme activity of 3-PGDH was measured by the method of Salach H. J. et al. (Method in Enzymology,

vol 9, 216-220 (1966)).

[0072] More specifically, 0.4 ml of 0.015 M NAD, 0.12 ml of 0.25 M EDTA (pH 9, NaOH), 0.1 ml of 0.05 M glutathione (pH 6, KOH), 0.5 ml of 1 M hydrazine (pH 9, acetate), 0.6 ml of 1 M Tris (pH 9, HCl), a suitable concentration of L-serine (0 to 40 mM), and water to make 2.3 ml, warmed to 25°C in advance, were added. Then, 0.2 ml of the crude enzyme solution was added and the temperature was kept the same for 5 minutes. Thereafter, 0.5 ml of 0.1 M 3-PGA (3-phosphoglycerate disodium salt, pH 7, NaOH) was added. After stirring, the absorbance at 340 nm of the reaction mixture was measured for 30 seconds. The reaction was carried out at 25°C.

[0073] For the measurement of activity, Hitachi U-2000A spectrophotometer was used.

[0074] Fig. 1 illustrates the results obtained. AJ13377 strain was relieved of L-serine sensitivity as compared with the wild type strain ATCC 14067. The AJ13324 strain was more relieved of L-serine sensitivity and the AJ13325 strain was of the same level as the AJ13324 strain in this respect. The AJ13327 strain was relieved of L-serine sensitivity greatly. And the inhibition was completely desensitized even in the presence of 80 mM L-serine.

[0075] Although some examples of desensitization of the inhibition of 3-PGDH by L-serine were reported on Escherichia coli (Tosa and Pizer, J. Bacteriol. 106: 972-982 (1971) or Japanese Patent Application Laid-open No. 6-510911), there has been known no example of complete desensitization of the inhibition in the presence of such a high concentration of L-serine.

(Example 5) Cloning of coryneform bacteria-derived wild type and mutant serA

[0076] As shown in Example 4, the feedback inhibition by L-serine was completely desensitized in the AJ13327 strain. Accordingly, cloning of serA gene coding for wild type 3-PGDH derived from the ATCC 14067 strain and mutant 3-PGDH derived from the AJ13327 strain was attempted in order to elucidate what the variation was like and confirm the amplification effect of 3-PGDH.

[0077] To amplify serA from the chromosome of Brevibacterium flavum using a PCR method, it is necessary to make a corresponding primer. Since no report has been made on the cloning and nucleotide sequence of serA of Brevibacterium flavum, the sequence of serA derived from Corynebacterium was used. Plasmid pDTS9901 was extracted from the strain Corynebacterium glutamicum K82 (cf. FERM BP-2444 and Japanese Patent Application Laid-open No. 3-7591) in which the serA fragment derived from Corynebacterium was cloned using Wizard Minipreps DNA Purification System (manufactured by Promega) and a DNA fragment of about 1.4 kb containing serA was cleaved with restriction enzyme BamHI (manufactured by Takara Shuzo Co., Ltd.).

[0078] As a vector for cloning the gene fragment, there was used a newly constructed cloning vector pVK7 for coryneform bacteria.

[0079] pVK7 was constructed by ligating (a cloning vector for Escherichia coli) pHSG299 (Kmr; Takeshita, S. et al., Gene, 61, 63-74 (1987), Japanese Patent Application Laid-open No. 10-215883), to pAM330, a cryptic plasmid of Brevibacterium lactofermentum, in the manner described below. pHSG299 was cleaved with monospecific restriction enzyme AvaII (manufactured by Takara Shuzo Co., Ltd.) and blunt ended with T4 DNA polymerase. This was ligated with pAM330 that had been cleaved with HindIII (manufactured by Takara Shuzo Co., Ltd.) and blunt ended with T4 DNA polymerase. The two types of plasmids obtained were designated pVK6 and pVK7 depending on the direction of pAM330 insertion relative to pHSG299, and pVK7 was used in the following experiments. pVK7 was capable of autonomous replication in Escherichia coli and Brevibacterium lactofermentum and retains the multiple cloning site and lacZ' derived from pHSG299. Fig. 2 illustrates the process of constructing pVK6 and pVK7.

[0080] To the shuttle vector pVK7 thus constructed was ligated a DNA fragment of about 1.4 kb containing serA. pDTS9901 was cleaved with restriction enzyme BamHI (manufactured by Takara Shuzo Co., Ltd.) and ligated to pVK7 also cleaved with restriction enzyme BamHI. The ligation of DNA was performed using DNA Ligation Kit (manufactured by Takara Shuzo Co., Ltd.) according to the prescribed method.

[0081] For the sequencing reaction, use was made of PCR thermal cycler MP type (manufactured by Takara Shuzo Co., Ltd.) and of Dye Terminator Cycle Sequencing FS Ready Reaction Kit (manufactured by Perkin Elmer). As the DNA primer, there were used M13(-21), RV primer (manufactured by Takara Shuzo Co., Ltd.). The SEQ ID NO : 1 in the Sequence Listing shows the sequence thus obtained. SEQ ID NO : 2 shows an amino acid sequence that can be coded for by this sequence.

[0082] A primer was synthesized based on the base sequence thus determined and serA was amplified by a PCR method using the chromosomal DNA of the mutant Brevibacterium flavum AJ13327 as a template. The SEQ ID NOS : 3 and 4 in the Sequence Listing show the N-terminal side and C terminal side sequences, respectively, of the DNA primer that were synthesized for gene amplification.

[0083] In the preparation of the chromosomal DNA of Brevibacterium flavum, use is made of Genomic DNA Purification Kit (Bacterial) (manufactured by Advanced Genetic Technologies Corp.) and the preparation method was according to the annexed protocol.

[0084] For the PCR reaction, use is made of PCR Thermal Cycler MP type (Takara Shuzo Co., Ltd.) and of TaKaRa

Taq (manufactured by Takara Shuzo Co., Ltd.).

[0085] The PCR product was ligated directly to plasmid pCR2.1 vector using Original TA Cloning Kit (manufactured by Invitrogen) and transformation was performed using competent cell of INVaF'. The transformed cells were spread on L medium (10 g/L of bactotryptone, 5 g/L of bactoyeast extract, 15 g/L of NaCl, and 15 g/L of agar) further containing 40 pg/ml of X-Gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside) and 25 pg/ml of Kanamycin, and incubated overnight. The white colonies, which appeared, were collected and separated to single colonies to obtain a transformed strain.

[0086] Plasmids were extracted from the transformed strain and those plasmids of which insertion of the serA fragment was confirmed by a PCR method were treated with restriction enzyme EcoRI and ligated to the shuttle vector pVK. Determination of the base sequence of the product suggested that no full-length sequence be contained on the C-terminal side. The sequence thus obtained corresponds to the region from 277 bases upstream of SEQ ID NO : 13 on the 5' side to the 1134th base of SEQ ID NO : 13 in the Sequence Listing on the 3' side.

[0087] To obtain a fragment containing the full length serA gene, cloning of a deleted part from the chromosomal DNA of Brevibacterium flavum AJ13327 strain was performed according to the annexed protocol using TaKaRa LA PCR in vitro Cloning Kit (manufactured by Takara Shuzo Co., Ltd.)

[0088] First, the chromosomal DNA thus prepared was completely digested with various restriction enzymes and ligated with cassettes having respective restriction enzyme sites corresponding thereto. Cassette primer (C1) (SEQ ID NO : 5 in the Sequence Listing) and a primer complementary to a known region of DNA (S1) (SEQ ID NO : 6 in the Sequence Listing) were used for carrying out first PCR. Using a portion of the reaction mixture, second PCR was carried out with inner primer C2 (SEQ ID NO : 7 in the Sequence Listing) and S2 (SEQ ID NO : 8 in the Sequence Listing) to amplify only the targeted DNA.

[0089] When EcoRI (manufactured by Takara Shuzo Co., Ltd.) was used as the restriction enzyme, the amplification of the targeted DNA was confirmed and the base sequence of the PCR product was determined directly. Based on the base sequence thus obtained, a primer coding for the C-terminal side was made and the fragments containing full length serA were collected from Brevibacterium flavum ATCC 14067 as a wild type strain and Brevibacterium flavum AJ13327 as a mutant strain. SEQ ID NOS : 9 and 10 in the Sequence Listing show the sequences of N-terminal and C-terminal side DNA primers, respectively.

[0090] The gene fragments containing wild type serA and mutant serA, respectively, in their full length were ligated to EcoRI-cleaved shuttle vector pVK7 using Original TA Cloning Kit (manufactured by Invitrogen). Plasmids harboring respective gene fragments were made separately and their base sequence was determined. SEQ ID NOS : 11 and 13 indicate the sequences of the wild type and of mutant, respectively. SEQ ID NOS : 12 and 14 indicate amino acid sequences that these sequences can code for. Comparing the base sequences thus determined, it was confirmed that in the mutant serA, the 1087th base, G, was mutated into A and as a result, the 325th amino acid, glutamic acid, was changed to lysine.

(Example 6) Introduction of Plasmid Containing 3-PGDH Gene into Brevibacterium flavum

[0091] Plasmids harboring wild type serA or mutant serA were each introduced into Brevibacterium flavum AJ13377. The plasmids were introduced by the electric pulse method (Sugimoto et al., Japanese Patent Application Laid-open No. 2-207791). Transformed cells were selected in a complete medium containing 25 pg/ml of kanamycin.

(Example 7) Production of L-serine by Transformed Cells

[0092] Transformed cells each having introduced therein plasmids harboring gene fragments containing wild serA or mutant serA in their full-length were incubated in a 500 ml shaking flask according to Example 3, and L-serine produced was determined. As a control, the AJ13377 strain as a host was incubated similarly.

[0093] In the transformed cell having introduced therein the wild type serA was observed no influence on its L-serine productivity whereas in the transformed cell having introduced therein the mutant serA was confirmed an increase in L-serine productivity (Table 3).

[0094] Brevibacterium flavum AJ13377 has been deposited since October 15, 1997 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology of Ministry of International Trade and Industry (zip code: 305-8566, 1-3 Higashi 1-Chome, Tsukuba-shi, Ibaraki-ken, Japan), as accession number of FERM P-16471, and transferred from the original deposition to international deposition based on Budapest Treaty on November 20, 1998, and has been deposited as accession number of FERM BP-6576.

[0095] Further, the plasmid containing the mutant serA was retained in Brevibacterium flavum ATCC 14067. The plasmid-retaining strain has been awarded Brevibacterium flavum AJ13378 and deposited since October 15, 1997 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology of Ministry of International Trade and Industry (zip code: 305-8566, 1-3 Higashi 1-Chome, Tsukuba-shi, Ibaraki-ken, Japan), as accession number of FERM P-16472, and transferred from the original deposition to international deposition based on

Budapest Treaty on November 20, 1998, and has been deposited as accession number of FERM BP-6577.

(Example 8) Amplification of serB and/or serC in Brevibacterium flavum L-serine Producing Strains

(1) Construction of Plasmid Expressing serB or serC

[0096] Plasmids pSB that express serB and plasmids pSC that express serC were constructed as illustrated in Figs. 3 and 4.

[0097] For the serB gene was made a primer (SEQ ID NOS : 15 and 16 in the Sequence Listing indicate N-terminal and C-terminal sides, respectively) based on the known base sequence (GenBank; X03046, M30784). On the other hand, for the serC gene, a primer (SEQ ID NOS : 17 and 18 in the Sequence Listing indicate N-terminal and C-terminal sides, respectively) was prepared based on the known base sequence (GenBank; D90728) and PCR was carried out using the chromosomal DNA of Escherichia coli JM109 as a template to obtain a gene fragment (1197 bp) containing ORF coding for serB and a gene fragment (1380 bp) containing ORF coding for serC.

[0098] The base sequences of SEQ ID NOS : 15 and 16 correspond to the regions of base Nos. 1197 to 1175 and of base Nos. 1 to 23 in the sequence GenBank; X03046, M30784 and the base sequences of SEQ ID NOS : 17 and 18 correspond to the regions of base Nos. 13205 to 13227 and of base Nos. 14584 to 14562 in the sequence GenBank; D90728.

[0099] The serB fragment, after blunt ended, was inserted into the SmaI site of pHSG399, a high copy type vector, to obtain p399B. To render this plasmid to be capable of autonomic replication in bacteria belonging to the genus Corynebacterium, a replicator (hereafter, referred to "Brev.-ori") was cleaved form pBK4 retaining the replicator derived from pHM1519 and inserted to p399B to obtain pSB (Fig. 3). pBK4 was made as follows. That is, a plasmid pHC4 containing Brev.-ori was prepared from Escherichia coli AJ12617 strain containing this plasmid (FERM BP-3532) and cleaved with KpnI (manufactured by Takara Shuzo Co., Ltd.) and BamHI (manufactured by Takara Shuzo Co., Ltd.) to extract Brev.-ori fragment, which was then blunt ended. Blunting of the ends was carried out using DNA Blunting Kit (manufactured by Takara Shuzo Co., Ltd.) according to the prescribed method. Thereafter, the product was ligated to an already phosphorylated BamHI linker and cleaved again with BamHI. This was ligated to pHSG298 that was also cleaved with BamHI to obtain pBK4. pBK4 may be used for cleaving Brev.-ori fragment with BamHI.

[0100] Further, a serC fragment was inserted to the SrfI site of pPCR-Script SK(+) to obtain pScript-serC. To the SacI site of the resulting plasmid was inserted a PstI linker. Then, the serC fragment was cleaved with PstI and inserted to the PstI site of pHSG399 to obtain p399C. A replicator was cleaved from pBK4 retaining the replicator derived from pHM1519 and inserted into p399C to obtain pSC (Fig. 4).

(2) Construction of Plasmid that Expresses serB and serC

[0101] Next, plasmids pBC8 and pBC14 that express serB and serC, respectively, were made (Fig. 5). To the SacI site existing outside the serC fragment of the above-described pScript-serC was inserted a PstI linker to introduce a PstI site. This plasmid was treated with PstI to cleave a serC fragment, which was then inserted to the PstI site of the serB-containing plasmid pSB. The base sequence was confirmed and the plasmid in which the serC fragment was inserted in the reverse direction to lacZ was named pBC8, and the plasmid in which it was inserted in the forward direction to lacZ was named pBC14.

(3) L-Serine Production by serB and serC Amplified Strains

[0102] Using the plasmids pSB, pSC and pBC8 made as described above, the wild type strain of Brevibacterium flavum ATCC 14067 was transformed and plasmids were extracted from the transformed cells. The plasmids were used for transforming Brevibacterium flavum AJ13377 and AJ13327 having L-serine productivity. Also, Brevibacterium flavum AJ13377 and AJ13327 strains retaining pBC8 were transformed with a plasmid containing the mutant serA that Brevibacterium flavum AJ13378 (FERM P-16472) retained.

[0103] Each of the transformed strains was incubated on an agar medium containing 10 mg/L of chloramphenicol and the colonies formed were each incubated in the same manner as in Example 3, followed by measurement of L-serine that accumulated in the medium. The transformed strains that contained mutant serA were incubated by adding 25 mg/L of kanamycin to the medium. Table 3 shows the results obtained.

Table 3

Strain	Amplified Gene	Amount of L-serine that accumulated (g/L)
AJ13377	-	5.0

Table 3 (continued)

Strain	Amplified Gene	Amount of L-serine that accumulated (g/L)
	serA	5.0
	serA*	12.0
	serB	19.3
	serC	8.3
	serB,serC	19.5
	serA*,serB,serC	24.8
AJ13327	-	15.4
	serB	24.2
	serC	19.8
	serB,serC	26.4
	serA*,serB,serC	35.2
serA*: Mutant serA gene		

[0104] As described above, amplification of serB or serC increased the amount of L-serine that accumulated. Also, amplification of the both serB and serC genes further increased the amount of L-serine that accumulated. In addition, amplification of the genes together with mutant serA gene increased the amount of L-serine that accumulated more. Similar results were obtained by using pBC14 instead of pBC8.

[0105] In the present example, although L-serine decomposing activity deficient strain (AJ13377) or L-serine decomposing activity deficient, azaserine resistant strain (AJ13327) of Brevibacterium flavum was used as coryneform bacterium host having L-serine productivity for amplifying each gene, other azaserine resistant strain (AJ13324) or L-serine decomposing activity deficient, β-(2-thienyl)-DL-alanine resistant strain (AJ13325) may also be used.

Annex to the description

[0106]

SEQUENCE LISTING

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Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
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Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
        275                 280                 285
Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys
    290                 295                 300
Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly
305                 310                 315                 320
Arg Val Gly Glu Glu Val Ala Val Trp Met Asp Leu Ala Arg Lys Leu
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Gly Leu Leu Ala Gly Lys Leu Val Asp
            340                 345
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gacgcggtcg tgcctgttgt aggcggacat tcctagtttt tccaggagta actt gtg 117
Val
1

agc cag aat ggc cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag 165
Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala Gln
5 10 15

tcc act gtt gac gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac 213
Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp
20 25 30

gga cct aac cgc cca gaa ctg ctt gat aca gtt aag gaa gcg gac gca 261
Gly Pro Asn Arg Pro Glu Leu Leu Asp Thr Val Lys Glu Ala Asp Ala
35 40 45

ctg ctc gtg cgt tct gct acc act gtc gat gct gaa gtc atc gcc gct 309
Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala
50 55 60 65

gcc cct aac ttg aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac 357
Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn
70 75 80

gtt gac atc cct gct gcc act gaa gct ggc gtc atg gtt gct aac gca 405
Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala
85 90 95

ccg acc tct aac att cac tct gct tgt gag cac gca att tct ttg ctg 453
Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu
100 105 110

ctg tct act gct cgc cag atc cct gct gct gat gcg acg ctg cgt gag 501

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Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg Glu
    115                 120                 125
ggc gag tgg aag cgg tct tct ttc aac ggt gtg gaa att ttc gga aaa   549
Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly Lys
130                 135                 140                 145
act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct cag   597
Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala Gln
                150                 155                 160
cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac gct   645
Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr Ala
            165                 170                 175
aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg gat   693
Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu Asp
        180                 185                 190
gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag acc   741
Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys Thr
    195                 200                 205
aag gaa act gct ggc atg ttt gat gcg cag ctc ctt gct aag tcc aag   789
Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser Lys
210                 215                 220                 225
aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat gaa   837
Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp Glu
                230                 235                 240
cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct ggt   885
Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala Gly
            245                 250                 255
ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc aag   933
Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe Lys
        260                 265                 270
ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa gag   981
Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu Glu
    275                 280                 285
gct cag gat cgt gcg ggt act gac gtt gct gat tct gtg ctc aag gcg   1029
Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys Ala
290                 295                 300                 305
ctg gct ggc gag ttc gtg gcg gat gct gtg aac gtt tcc ggt ggt cgc   1077
Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly Arg
                310                 315                 320
gtg ggc gaa gag gtt gct gtg tgg atg gat ctg gct cgc aag ctt ggt   1125
Val Gly Glu Glu Val Ala Val Trp Met Asp Leu Ala Arg Lys Leu Gly
            325                 330                 335
ctt ctt gct ggc aag ctt gtc gac gcc gcc cca gtc tcc att gag gtt   1173
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Leu Leu Ala Gly Lys Leu Val Asp Ala Ala Pro Val Ser Ile Glu Val
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gag gct cga ggc gag ctt tct tcc gag cag gtc gat gca ctt ggt ttg   1221
Glu Ala Arg Gly Glu Leu Ser Ser Glu Gln Val Asp Ala Leu Gly Leu
    355                 360                 365
tcc gct gtt cgt ggt ttg ttc tcc gga att atc gaa gag tcc gtt act   1269
Ser Ala Val Arg Gly Leu Phe Ser Gly Ile Ile Glu Glu Ser Val Thr
370                 375                 380                 385
ttc gtc aac gct cct cgc att gct gaa gag cgt ggc ctg gac atc tcc   1317
Phe Val Asn Ala Pro Arg Ile Ala Glu Glu Arg Gly Leu Asp Ile Ser
                390                 395                 400
gtg aag acc aac tct gag tct gtt act cac cgt tcc gtc ctg cag gtc   1365
Val Lys Thr Asn Ser Glu Ser Val Thr His Arg Ser Val Leu Gln Val
            405                 410                 415
aag gtc att act ggc agc ggc gcg agc gca act gtt gtt ggt gcc ctg   1413
Lys Val Ile Thr Gly Ser Gly Ala Ser Ala Thr Val Val Gly Ala Leu
        420                 425                 430
act ggt ctt gag cgc gtt gag aag atc acc cgc atc aat ggc cgt ggc   1461
Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile Asn Gly Arg Gly
    435                 440                 445
ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg cag tac act gac   1509
Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu Gln Tyr Thr Asp
450                 455                 460                 465
gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg ggt gct gct ggc   1557
Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu Gly Ala Ala Gly
                470                 475                 480
atc aac atc gag gct gct gcg ttg act cag gct gag aag ggt gac ggc   1605
Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu Lys Gly Asp Gly
            485                 490                 495
gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tcc gaa gag ctg gaa   1653
Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser Glu Glu Leu Glu
        500                 505                 510
gct gaa atc aac gct gag ttg ggt gct act tcc ttc cag gtt gat ctt   1701
Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe Gln Val Asp Leu
    515                 520                 525
gac taattagaga tccattttct agaacc                                  1730
Asp
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            20                  25                  30
Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Thr Val Lys Glu Ala Asp
        35                  40                  45
Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
    50                  55                  60
Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
65                  70                  75                  80
Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
                85                  90                  95
Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
            100                 105                 110
Leu Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg
        115                 120                 125
Glu Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly
    130                 135                 140
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
145                 150                 155                 160
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
                165                 170                 175
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
            180                 185                 190
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
        195                 200                 205
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser
    210                 215                 220
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
225                 230                 235                 240
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
                245                 250                 255
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
            260                 265                 270
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
        275                 280                 285
Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys
    290                 295                 300
Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly
305                 310                 315                 320
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Arg Val Gly Glu Glu Val Ala Val Trp Met Asp Leu Ala Arg Lys Leu
                325                 330                 335
Gly Leu Leu Ala Gly Lys Leu Val Asp Ala Ala Pro Val Ser Ile Glu
            340                 345                 350
Val Glu Ala Arg Gly Glu Leu Ser Ser Glu Gln Val Asp Ala Leu Gly
        355                 360                 365
Leu Ser Ala Val Arg Gly Leu Phe Ser Gly Ile Ile Glu Glu Ser Val
    370                 375                 380
Thr Phe Val Asn Ala Pro Arg Ile Ala Glu Glu Arg Gly Leu Asp Ile
385                 390                 395                 400
Ser Val Lys Thr Asn Ser Glu Ser Val Thr His Arg Ser Val Leu Gln
                405                 410                 415
Val Lys Val Ile Thr Gly Ser Gly Ala Ser Ala Thr Val Val Gly Ala
            420                 425                 430
Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile Asn Gly Arg
        435                 440                 445
Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu Gln Tyr Thr
    450                 455                 460
Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu Gly Ala Ala
465                 470                 475                 480
Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu Lys Gly Asp
                485                 490                 495
Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser Glu Glu Leu
            500                 505                 510
Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe Gln Val Asp
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Leu Asp
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gacgcggtcg tgcctgttgt aggcggacat tcctagtttt tccaggagta actt gtg   117
                                                            Val
                                                             1
agc cag aat ggc cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag   165
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```
Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala Gln
                5                  10                  15
tcc act gtt gac gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac   213
Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp
         20                  25                  30
gga cct aac cgc cca gaa ctg ctt gat aca gtt aag gaa gcg gac gca   261
Gly Pro Asn Arg Pro Glu Leu Leu Asp Thr Val Lys Glu Ala Asp Ala
     35                  40                  45
ctg ctc gtg cgt tct gct acc act gtc gat gct gaa gtc atc gcc gct   309
Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala
 50                  55                  60                  65
gcc cct aac ttg aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac   357
Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn
                70                  75                  80
gtt gac atc cct gct gcc act gaa gct ggc gtc atg gtt gct aac gca   405
Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala
             85                  90                  95
ccg acc tct aac att cac tct gct tgt gag cac gca att tct ttg ctg   453
Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu
        100                 105                 110
ctg tct act gct cgc cag atc cct gct gct gat gcg acg ctg cgt gag   501
Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg Glu
    115                 120                 125
ggc gag tgg aag cgg tct tct ttc aac ggt gtg gaa att ttc gga aaa   549
Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly Lys
130                 135                 140                 145
act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct cag   597
Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala Gln
                150                 155                 160
cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac gct   645
Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr Ala
            165                 170                 175
aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg gat   693
Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu Asp
        180                 185                 190
gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag acc   741
Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys Thr
    195                 200                 205
aag gaa act gct ggc atg ttt gat gcg cag ctc ctt gct aag tcc aag   789
Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser Lys
210                 215                 220                 225
aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat gaa   837
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Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp Glu
                230                 235                 240
cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct ggt   885
Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala Gly
            245                 250                 255
ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc aag   933
Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe Lys
        260                 265                 270
ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa gag   981
Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu Glu
    275                 280                 285
gct cag gat cgt gcg ggt act gac gtt gct gat tct gtg ctc aag gcg   1029
Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys Ala
290                 295                 300                 305
ctg gct ggc gag ttc gtg gcg gat gct gtg aac gtt tcc ggt ggt cgc   1077
Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly Arg
                310                 315                 320
gtg ggc gaa aag gtt gct gtg tgg atg gat ctg gct cgc aag ctt ggt   1125
Val Gly Glu Lys Val Ala Val Trp Met Asp Leu Ala Arg Lys Leu Gly
            325                 330                 335
ctt ctt gct ggc aag ctt gtc gac gcc gcc cca gtc tcc att gag gtt   1173
Leu Leu Ala Gly Lys Leu Val Asp Ala Ala Pro Val Ser Ile Glu Val
        340                 345                 350
gag gct cga ggc gag ctt tct tcc gag cag gtc gat gca ctt ggt ttg   1221
Glu Ala Arg Gly Glu Leu Ser Ser Glu Gln Val Asp Ala Leu Gly Leu
    355                 360                 365
tcc gct gtt cgt ggt ttg ttc tcc gga att atc gaa gag tcc gtt act   1269
Ser Ala Val Arg Gly Leu Phe Ser Gly Ile Ile Glu Glu Ser Val Thr
370                 375                 380                 385
ttc gtc aac gct cct cgc att gct gaa gag cgt ggc ctg gac atc tcc   1317
Phe Val Asn Ala Pro Arg Ile Ala Glu Glu Arg Gly Leu Asp Ile Ser
                390                 395                 400
gtg aag acc aac tct gag tct gtt act cac cgt tcc gtc ctg cag gtc   1365
Val Lys Thr Asn Ser Glu Ser Val Thr His Arg Ser Val Leu Gln Val
            405                 410                 415
aag gtc att act ggc agc ggc gcg agc gca act gtt gtt ggt gcc ctg   1413
Lys Val Ile Thr Gly Ser Gly Ala Ser Ala Thr Val Val Gly Ala Leu
        420                 425                 430
act ggt ctt gag cgc gtt gag aag atc acc cgc atc aat ggc cgt ggc   1461
Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile Asn Gly Arg Gly
    435                 440                 445
ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg cag tac act gac   1509
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Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu Gln Tyr Thr Asp
450                 455                 460                 465
gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg ggt gct gct ggc   1557
Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu Gly Ala Ala Gly
            470                 475                 480
atc aac atc gag gct gct gcg ttg act cag gct gag aag ggt gac ggc   1605
Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu Lys Gly Asp Gly
        485                 490                 495
gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tcc gaa gag ctg gaa   1653
Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser Glu Glu Leu Glu
    500                 505                 510
gct gaa atc aac gct gag ttg ggt gct act tcc ttc cag gtt gat ctt   1701
Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe Gln Val Asp Leu
515                 520                 525
gac taattagaga tccatttttct agaacc                                 1730
Asp
530
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<212> PRT
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<400> 14

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             20                  25                  30
Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Thr Val Lys Glu Ala Asp
         35                  40                  45
Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
     50                  55                  60
Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65                  70                  75                  80
Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
                 85                  90                  95
Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
            100                 105                 110
Leu Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg
        115                 120                 125
Glu Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly
    130                 135                 140
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
```

```
145                 150                 155                 160
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
                165                 170                 175
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
            180                 185                 190
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
        195                 200                 205
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser
    210                 215                 220
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
225                 230                 235                 240
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
                245                 250                 255
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
            260                 265                 270
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
        275                 280                 285
Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys
    290                 295                 300
Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly
305                 310                 315                 320
Arg Val Gly Glu Lys Val Ala Val Trp Met Asp Leu Ala Arg Lys Leu
                325                 330                 335
Gly Leu Leu Ala Gly Lys Leu Val Asp Ala Ala Pro Val Ser Ile Glu
            340                 345                 350
Val Glu Ala Arg Gly Glu Leu Ser Ser Glu Gln Val Asp Ala Leu Gly
        355                 360                 365
Leu Ser Ala Val Arg Gly Leu Phe Ser Gly Ile Ile Glu Glu Ser Val
    370                 375                 380
Thr Phe Val Asn Ala Pro Arg Ile Ala Glu Glu Arg Gly Leu Asp Ile
385                 390                 395                 400
Ser Val Lys Thr Asn Ser Glu Ser Val Thr His Arg Ser Val Leu Gln
                405                 410                 415
Val Lys Val Ile Thr Gly Ser Gly Ala Ser Ala Thr Val Val Gly Ala
            420                 425                 430
Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile Asn Gly Arg
        435                 440                 445
Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu Gln Tyr Thr
    450                 455                 460
Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu Gly Ala Ala
465                 470                 475                 480
Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu Lys Gly Asp
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485 490 495

Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser Glu Glu Leu
500 505 510
Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe Gln Val Asp
515 520 525
Leu Asp
530

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<210> 18
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<400> 18

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Claims

1. A coryneform bacterium having L-serine productivity in which an activity of at least one of phosphoserine phosphatase and phosphoserine transaminase is enhanced.

2. The coryneform bacterium as claimed in claim 1, wherein said bacterium is enhanced the activities of both phosphoserine phosphatase and phosphoserine transaminase.

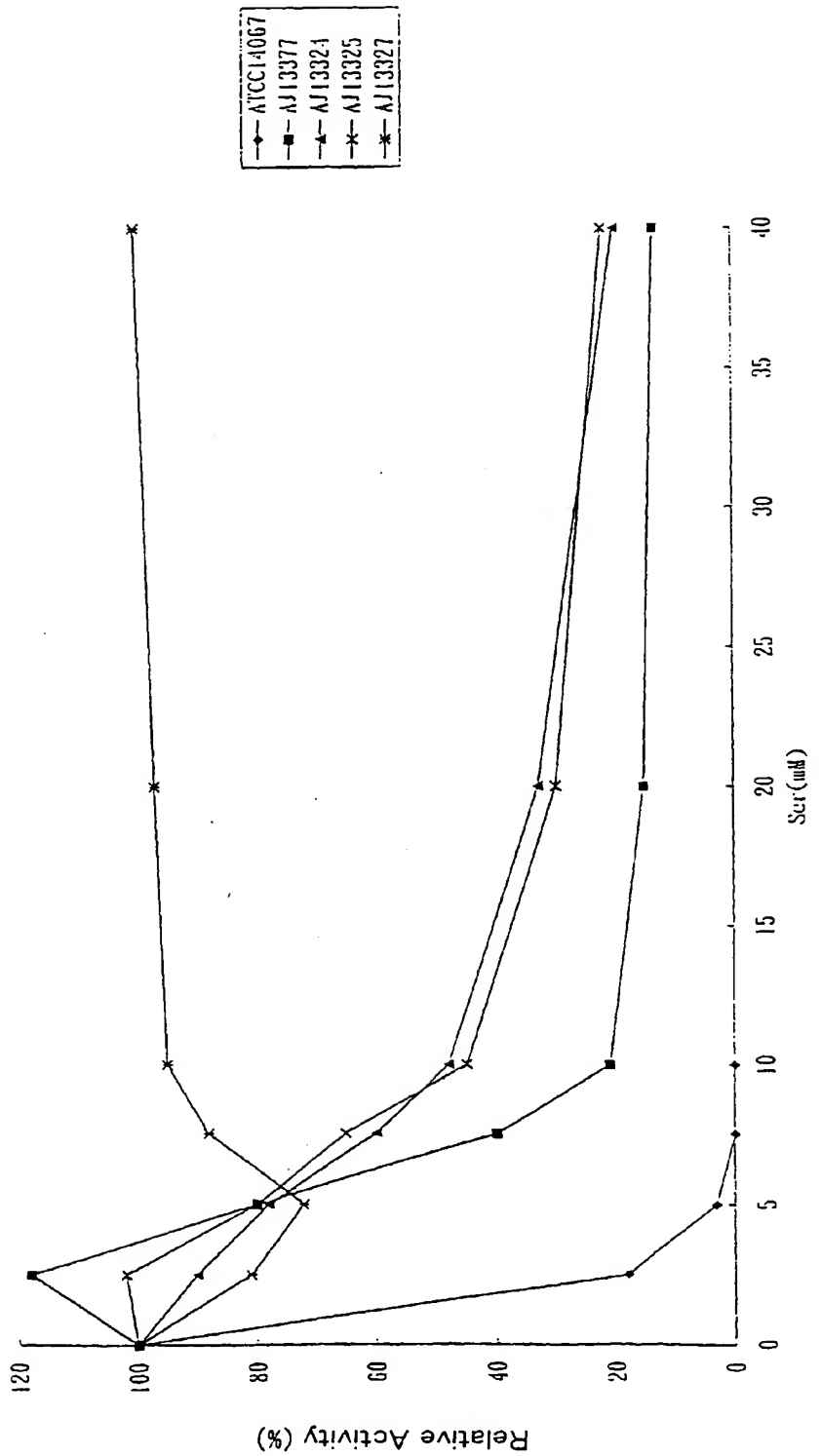
3. The coryneform bacterium as claimed in claim 1, wherein said bacterium has L-serine productivity due to deficiency in L-serine decomposing activity.

4. The coryneform bacterium as claimed in claim 1 or 3, wherein said bacterium has L-serine productivity due to its resistance to L-serine analogue(s).

5. The coryneform bacterium as claimed in claim 1, wherein an activity of phosphoserine phosphatase or phosphoserine transaminase is enhanced by increasing a copy number of a gene coding for phosphoserine phosphatase or a gene coding for phosphoserine transaminase in said coryneform bacterium in its cell.

6. The coryneform bacterium as claimed in any one of claims 1 to 5, wherein said bacterium has introduced therein a gene coding for D-3-phosophoglycerate dehydrogenase in which feedback inhibition by L-serine is desensitized.

7. A method of producing L-serine, comprising the steps of cultivating the coryneform bacterium as claimed in any one of claims 1 to 6 in a medium to accumulate L-serine in the medium and collecting the L-serine from the medium.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AJ13321
AJ13325
AJ13327
Relative Activity (%)
120
100
80
60
40
20
0
0
5
10
15
20
25
30
35
40
Ser(mM)

FIG. 1

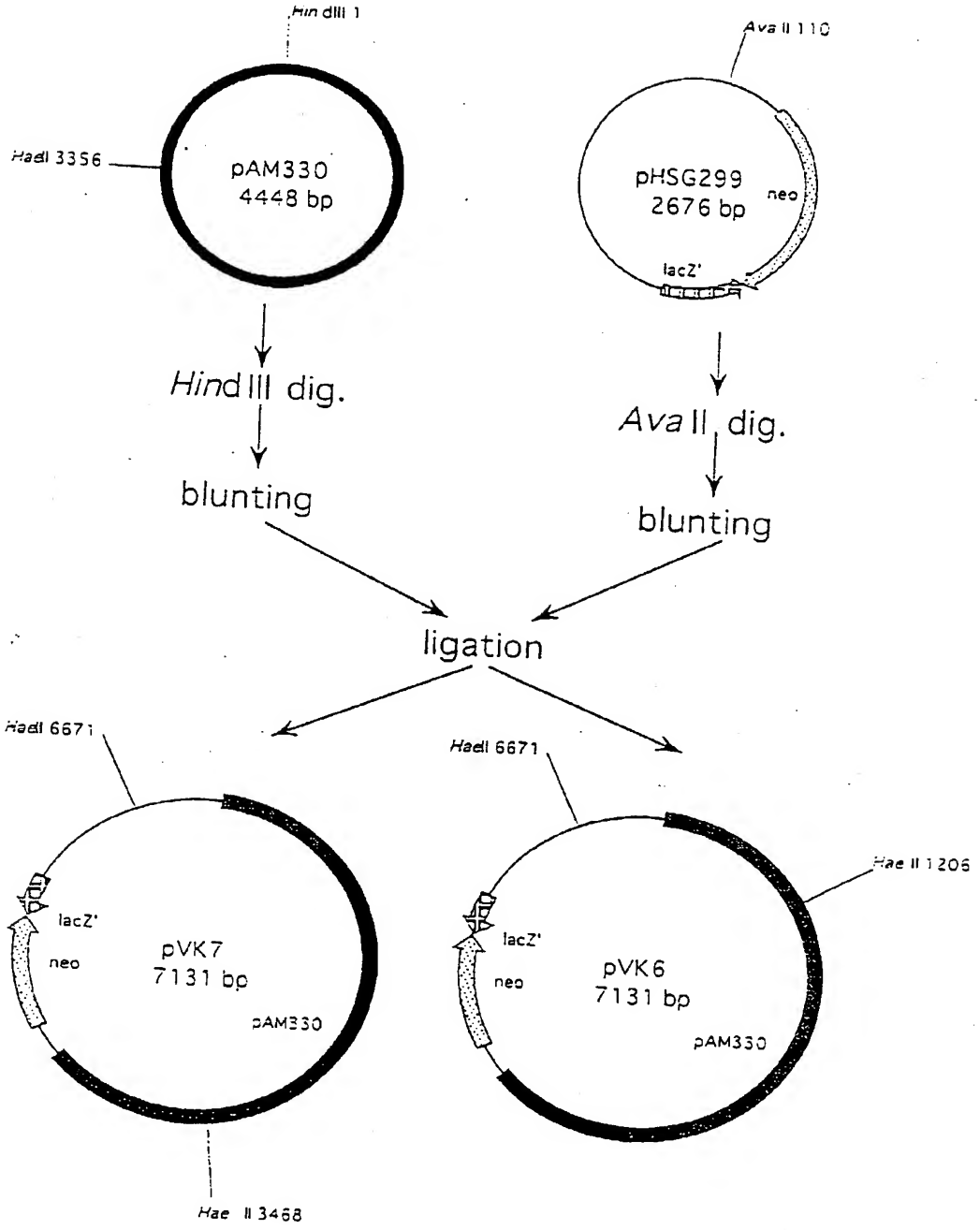
Hin dIII 1
HaeI 3356
pAM330
4448 bp
Hind III dig.
blunting
Ava II 110
pHSG299
2676 bp
neo
lacZ'
Ava II dig.
blunting
ligation
HaeI 6671
lacZ'
neo
pVK7
7131 bp
pAM330
Hae II 3468
HaeI 6671
lacZ'
neo
pVK6
7131 bp
pAM330
Hae II 1206

FIG. 2

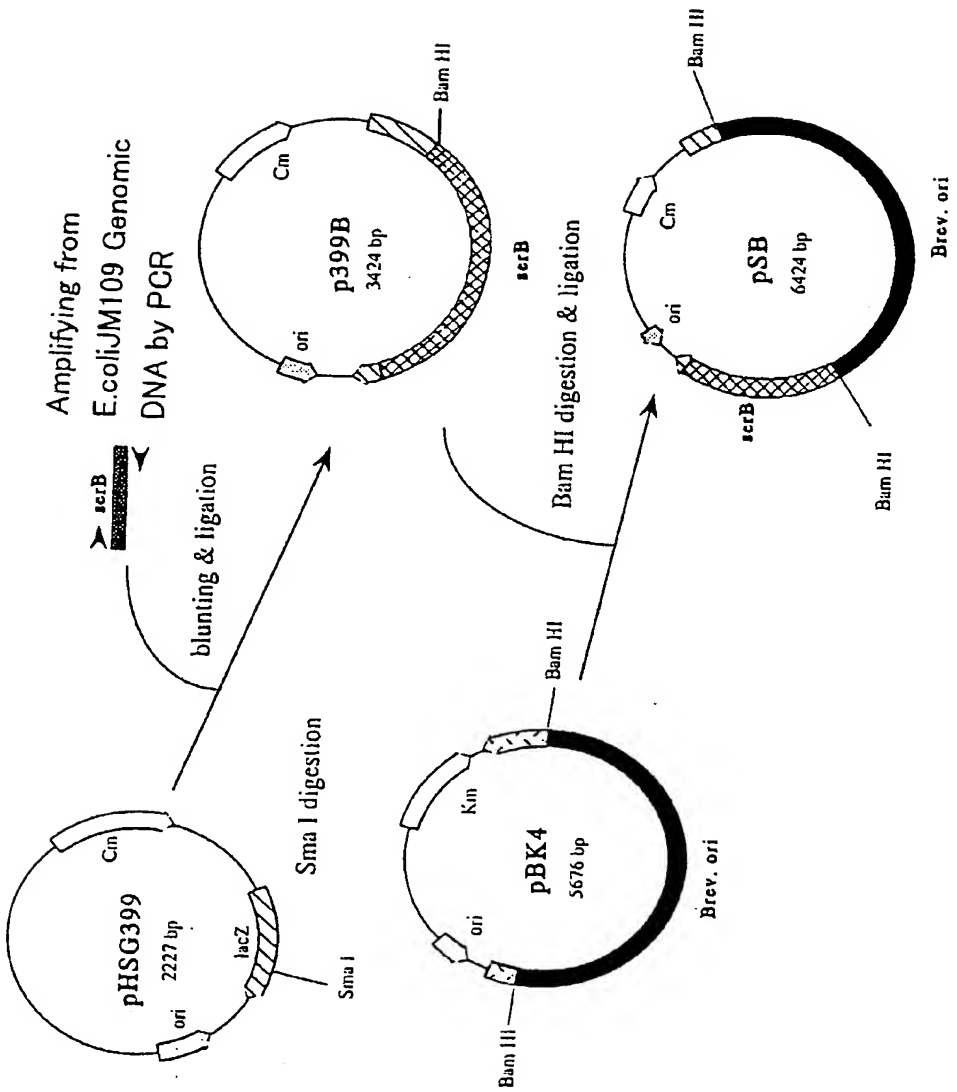
Amplifying from
E.coliJM109 Genomic
DNA by PCR
scrB
blunting & ligation
Sma I digestion
pHSG399
2227 bp
Cm
ori
lacZ
Sma I
p399B
3424 bp
Cm
ori
Bam HI
scrB
Bam HI digestion & ligation
pBK4
5676 bp
Km
ori
Brev. ori
Bam HI
Bam HI
pSB
6424 bp
Cm
ori
scrB
Brev. ori
Bam HI

FIG. 3

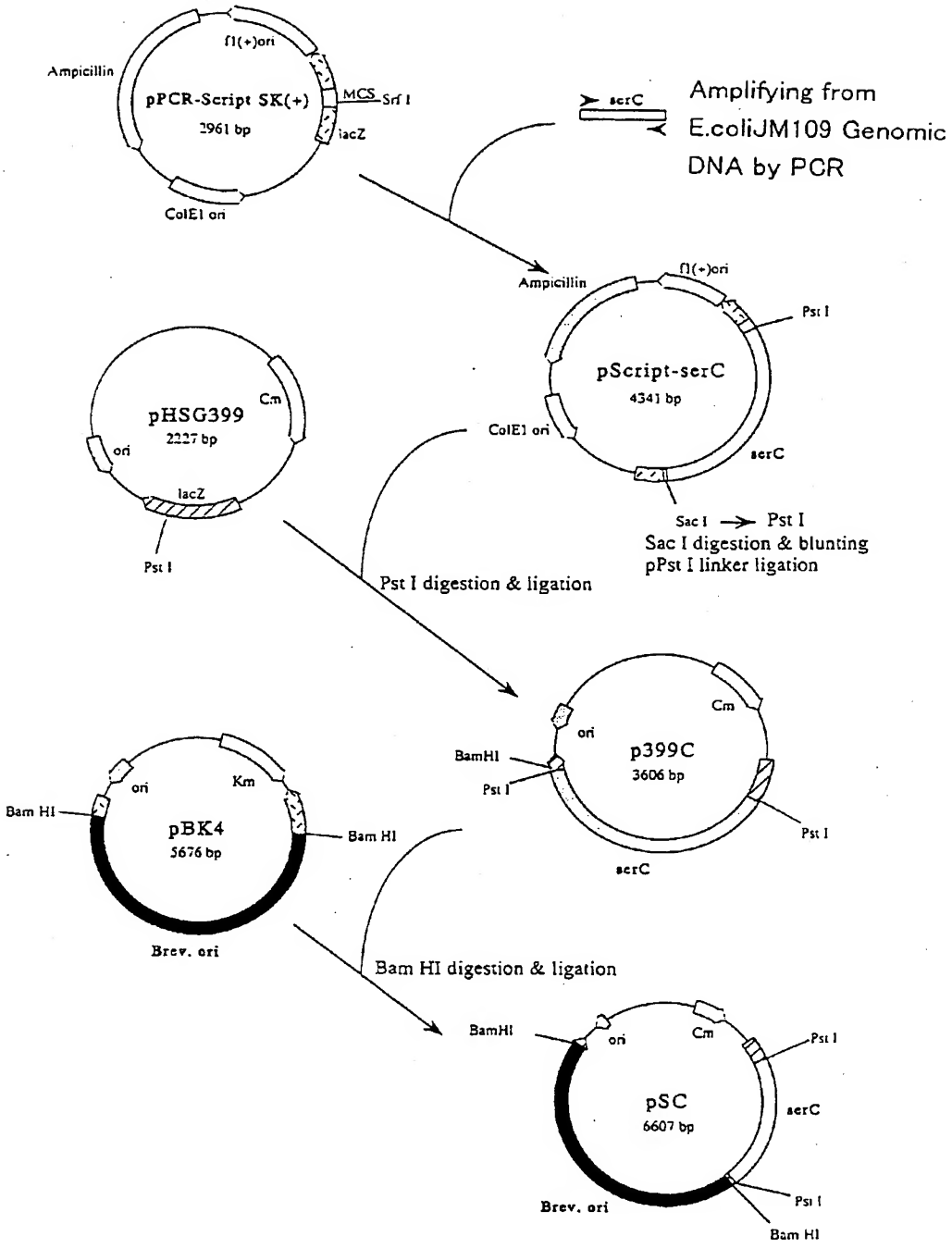
Ampicillin
f1(+)ori
pPCR-Script SK(+)
2961 bp
MCS
Srf I
lacZ
ColE1 ori
serC
Amplifying from
E.coliJM109 Genomic
DNA by PCR
Ampicillin
f1(+)ori
Pst I
pScript-serC
4341 bp
ColE1 ori
serC
Sac I → Pst I
Sac I digestion & blunting
pPst I linker ligation
pHSG399
2227 bp
Cm
ori
lacZ
Pst I
Pst I digestion & ligation
Cm
ori
BamHI
Pst I
p399C
3606 bp
Pst I
serC
ori
Km
Bam HI
pBK4
5676 bp
Bam HI
Brev. ori
Bam HI digestion & ligation
BamHI
ori
Cm
Pst I
pSC
6607 bp
serC
Pst I
Brev. ori
Bam HI

FIG. 4

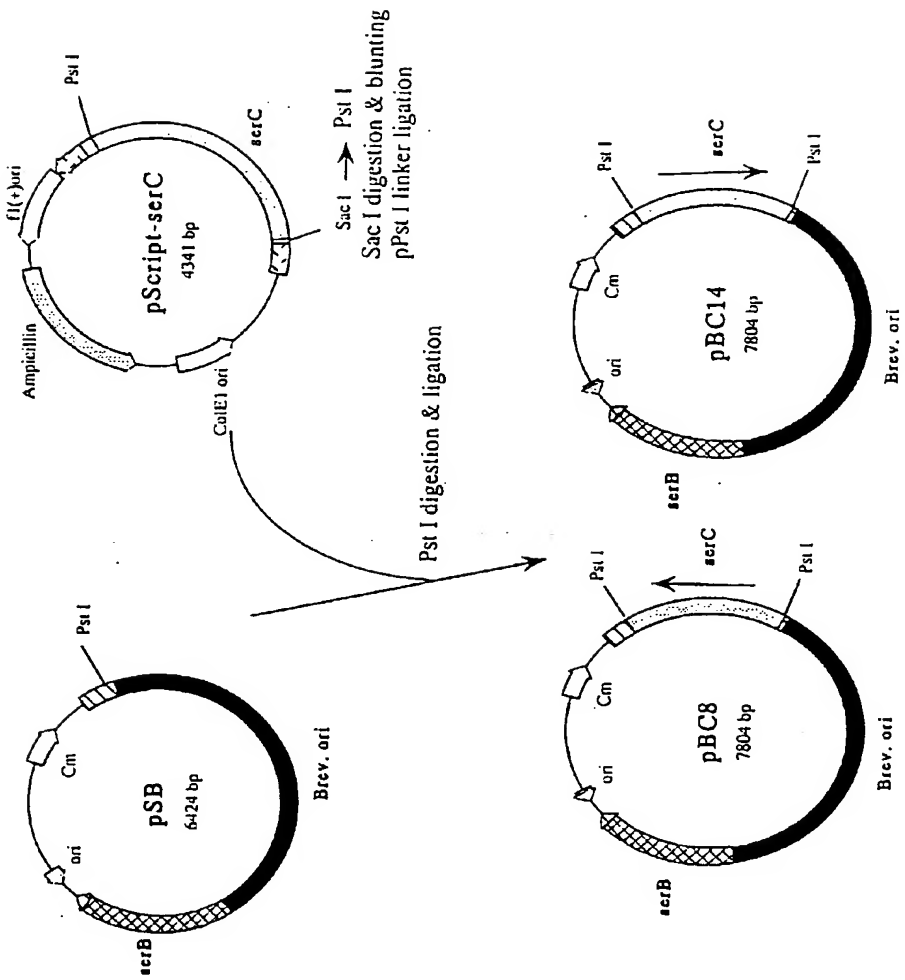
Pst I
fl(+)ori
pScript-serC
4341 bp
serC
Ampicillin
ColE1 ori
Sac I → Pst I
Sac I digestion & blunting
pPst I linker ligation
Pst I digestion & ligation
pSB
6424 bp
Cm
ori
serB
Brev. ori
pBC14
7804 bp
pBC8
7804 bp

FIG. 5